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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2		"Ask CAS" for self-help around the clock
NEWS 3	DEC 23	New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/ USPAT2
NEWS 4	JAN 13	IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
NEWS 5	JAN 13	New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to INPADOC
NEWS 6	JAN 17	Pre-1988 INPI data added to MARPAT
NEWS 7	JAN 17	IPC 8 in the WPI family of databases including WPIFV
NEWS 8	JAN 30	Saved answer limit increased
NEWS 9	FEB 21	STN AnaVist, Version 1.1, lets you share your STN AnaVist visualization results
NEWS 10	FEB 22	The IPC thesaurus added to additional patent databases on STN
NEWS 11	FEB 22	Updates in EPFULL; IPC 8 enhancements added
NEWS 12	FEB 27	New STN AnaVist pricing effective March 1, 2006
NEWS 13	FEB 28	MEDLINE/LMEDLINE reload improves functionality
NEWS 14	FEB 28	TOXCENTER reloaded with enhancements
NEWS 15	FEB 28	REGISTRY/ZREGISTRY enhanced with more experimental spectral property data
NEWS 16	MAR 01	INSPEC reloaded and enhanced
NEWS 17	MAR 03	Updates in PATDPA; addition of IPC 8 data without attributes
NEWS 18	MAR 08	X.25 communication option no longer available after June 2006
NEWS 19	MAR 22	EMBASE is now updated on a daily basis
NEWS 20	APR 03	New IPC 8 fields and IPC thesaurus added to PATDPAFULL
NEWS 21	APR 03	Bibliographic data updates resume; new IPC 8 fields and IPC thesaurus added in PCTFULL
NEWS 22	APR 04	STN AnaVist $500 visualization usage credit offered

NEWS EXPRESS FEBRUARY 15 CURRENT VERSION FOR WINDOWS IS V8.01a,
CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
V8.0 AND V8.01 USERS CAN OBTAIN THE UPGRADE TO V8.01a AT
http://download.cas.org/express/v8.0-Discover/

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* * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 14:36:36 ON 10 APR 2006

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=> file .cluster1
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

FILE 'MEDLINE' ENTERED AT 14:37:07 ON 10 APR 2006

FILE 'AGRICOLA' ENTERED AT 14:37:07 ON 10 APR 2006

FILE 'CABA' ENTERED AT 14:37:07 ON 10 APR 2006
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FILE 'CAPLUS' ENTERED AT 14:37:07 ON 10 APR 2006
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FILE 'EMBASE' ENTERED AT 14:37:07 ON 10 APR 2006
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=> rat and genome and draft
L1          152 RAT AND GENOME AND DRAFT

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2           49 DUP REM L1 (103 DUPLICATES REMOVED)

=> l2 and PY<2002
   1 FILES SEARCHED...
   5 FILES SEARCHED...
L3            7 L2 AND PY<2002

=> d l3 1- ti
YOU HAVE REQUESTED DATA FROM 7 ANSWERS - CONTINUE? Y/(N):y

L3   ANSWER 1 OF 7     MEDLINE on STN
TI   DNA methylation and Z-DNA formation as mediators of quantitative
     differences in the expression of alleles.

L3   ANSWER 2 OF 7     MEDLINE on STN
TI   A genomic-systems biology map for cardiovascular function.

L3   ANSWER 3 OF 7     MEDLINE on STN
TI   Using PAC nested deletions to order contigs and microsatellite markers at
     the high repetitive sequence containing Npr3 gene locus.

L3   ANSWER 4 OF 7     MEDLINE on STN
TI   Comparative physical mapping of targeted regions of the rat
     genome.

L3   ANSWER 5 OF 7     MEDLINE on STN
TI   Mapping and identification of autoimmunity genes.

L3   ANSWER 6 OF 7     MEDLINE on STN
TI   Shotgun sample sequence comparisons between mouse and human
     genomes.
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L3   ANSWER 7 OF 7  BIOSIS  COPYRIGHT (c) 2006 The Thomson Corporation  on STN
TI   Segmental duplications: What's missing, misassigned, and misassembled-and
     should we care?.


=> rat and ESTs and 20000
L4            0 RAT AND ESTS AND 20000

=> rat and ESTs and genome
L5          359 RAT AND ESTS AND GENOME

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6          114 DUP REM L5 (245 DUPLICATES REMOVED)

=> l6 and py<2002
   1 FILES SEARCHED...
   5 FILES SEARCHED...
L7           44 L6 AND PY<2002

=> d l7 1-10 ti

L7   ANSWER 1 OF 44      MEDLINE on STN
TI   Human proton/oligopeptide transporter (POT) genes: identification of
     putative human genes using bioinformatics.

L7   ANSWER 2 OF 44      MEDLINE on STN
TI   Automated construction of high-density comparative maps between
     rat, human, and mouse.

L7   ANSWER 3 OF 44      MEDLINE on STN
TI   Mouse BAC ends quality assessment and sequence analyses.

L7   ANSWER 4 OF 44      MEDLINE on STN
TI   A radiation hybrid transcript map of the mouse genome.

L7   ANSWER 5 OF 44      MEDLINE on STN
TI   Identification of differential gene expression profiles in rat
     cortical cells exposed to the neuroactive agents trimethylolpropane
     phosphate and bicuculline.

L7   ANSWER 6 OF 44      MEDLINE on STN
TI   Generation of a high-density rat EST map.

L7   ANSWER 7 OF 44      MEDLINE on STN
TI   Differentially expressed endoderm and mesenchyme genes along the fetal
     rat intestine.

L7   ANSWER 8 OF 44      MEDLINE on STN
TI   Cloning and characterization of 13 novel transcripts and the human RGS8
     gene from the 1q25 region encompassing the hereditary prostate cancer
     (HPC1) locus.

L7   ANSWER 9 OF 44      MEDLINE on STN
TI   Gene index analysis of the human genome estimates approximately
     120,000 genes.

L7   ANSWER 10 OF 44      MEDLINE on STN
TI   Comparative gene mapping workshop: progress in agriculturally important
     animals.


=> d l7 6 ibib abs
```

L7 ANSWER 6 OF 44 MEDLINE on STN
ACCESSION NUMBER: 2001354684 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11230173
TITLE: Generation of a high-density **rat** EST map.
AUTHOR: Scheetz T E; Raymond M R; Nishimura D Y; McClain A; Roberts C; Birkett C; Gardiner J; Zhang J; Butters N; Sun C; Kwitek-Black A; Jacob H; Casavant T L; Soares M B; Sheffield V C
CORPORATE SOURCE: Howard Hughes Medical Institute, University of Iowa, Iowa City, Iowa 52242, USA.
CONTRACT NUMBER: 2R01HL59789 (NHLBI)
SOURCE: Genome research, **(2001 Mar)** Vol. 11, No. 3, pp. 497-502.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010625
Last Updated on STN: 20010625
Entered Medline: 20010621
AB We have developed a high-density EST map of the **rat**, consisting of >11,000 **ESTs**. These **ESTs** were placed on a radiation hybrid framework map of genetic markers spanning all 20 **rat** autosomes, plus the X chromosome. The framework maps have a total size of approximately 12,400 cR, giving an average correspondence of 240 kb/cR. The frameworks are all LOD 3 chromosomal maps consisting of 775 radiation-hybrid-mapped genetic markers and **ESTs**. To date, we have generated radiation-hybrid-mapping data for >14,000 novel **ESTs** identified by our **Rat** Gene Discovery and Mapping Project (http://ratEST.uiowa.edu), from which we have placed >11,000 on our framework maps. To minimize mapping errors, **ESTs** were mapped in duplicate and consensus RH vectors produced for use in the placement procedure. This EST map was then used to construct high-density comparative maps between **rat** and human and **rat** and mouse. These maps will be a useful resource for positional cloning of genes for **rat** models of human diseases and in the creation and verification of a tiling set of map order for the upcoming **rat-genome** sequencing.

=> FIL STNGUIDE
COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION
FULL ESTIMATED COST 41.44 41.65

FILE 'STNGUIDE' ENTERED AT 14:58:15 ON 10 APR 2006
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FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Apr 7, 2006 (20060407/UP).

=> rat genome u34
1 RAT
1 GENOME
0 U34
L8 0 RAT GENOME U34
(RAT(W)GENOME(W)U34)

=> file .cluster1
COST IN U.S. DOLLARS SINCE FILE TOTAL

	ENTRY	SESSION
FULL ESTIMATED COST	0.96	42.61

FILE 'MEDLINE' ENTERED AT 15:07:38 ON 10 APR 2006

FILE 'AGRICOLA' ENTERED AT 15:07:38 ON 10 APR 2006

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=> rat genome u34
L9 16 RAT GENOME U34

=> d l9 ibib abs

L9 ANSWER 1 OF 16 MEDLINE on STN
ACCESSION NUMBER: 2004198669 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15093671
TITLE: Effect of serum cholesterol on the mRNA content of amyloid precursor protein in rat livers.
AUTHOR: Kiyosawa Naoki; Ito Kazumi; Niino Noriyo; Sakuma Kyoko; Kanbori Miyuki; Yamoto Takashi; Manabe Sunao; Matsunuma Naochika
CORPORATE SOURCE: Medicinal Safety Research Labs., Sankyo Co. Ltd., 717 Horikoshi, Fukuroi, Shizuoka 437-0065, Japan.. kiyosawa@fuku.sankyo.co.jp
SOURCE: Toxicology letters, (2004 Apr 21) Vol. 150, No. 2, pp. 157-66.
Journal code: 7709027. ISSN: 0378-4274.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200405
ENTRY DATE: Entered STN: 20040420
Last Updated on STN: 20040521
Entered Medline: 20040520

AB Genes that showed mRNA content profiles, which correlated with serum concentrations of total cholesterol (T.CHO), were screened from the microarray data of phenobarbital (PB)- or clofibrate (CLO)-treated rat livers, and the correlation was evaluated based on Spearman's correlation coefficient. Many genes involved in the cholesterol or bile acid metabolism were highly correlated such as UDP-glucuronosyltransferase-21, apolipoprotein A-I and cMOAT. The mRNA content of the amyloid precursor protein (APP) showed the 5th highest correlation among the 8799 probes in the Affymetrix **Rat Genome U34** Array. In the livers of rats fed a high-cholesterol (1%) diet for 33 days, serum T.CHO levels increased by 4.6-fold, and the hepatic APP mRNA content also increased by 1.9-fold compared to the control group. These data suggest that the hepatic APP mRNA content was affected by serum T.CHO, and that

hepatic APP was involved in cholesterol metabolism in rat livers.

=> d l9 1- ibib abs
YOU HAVE REQUESTED DATA FROM 16 ANSWERS - CONTINUE? Y/(N):y

L9 ANSWER 1 OF 16 MEDLINE on STN
ACCESSION NUMBER: 2004198669 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15093671
TITLE: Effect of serum cholesterol on the mRNA content of amyloid precursor protein in rat livers.
AUTHOR: Kiyosawa Naoki; Ito Kazumi; Niino Noriyo; Sakuma Kyoko; Kanbori Miyuki; Yamoto Takashi; Manabe Sunao; Matsunuma Naochika
CORPORATE SOURCE: Medicinal Safety Research Labs., Sankyo Co. Ltd., 717 Horikoshi, Fukuroi, Shizuoka 437-0065, Japan.. kiyosawa@fuku.sankyo.co.jp
SOURCE: Toxicology letters, (2004 Apr 21) Vol. 150, No. 2, pp. 157-66.
Journal code: 7709027. ISSN: 0378-4274.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200405
ENTRY DATE: Entered STN: 20040420
Last Updated on STN: 20040521
Entered Medline: 20040520

AB Genes that showed mRNA content profiles, which correlated with serum concentrations of total cholesterol (T.CHO), were screened from the microarray data of phenobarbital (PB)- or clofibrate (CLO)-treated rat livers, and the correlation was evaluated based on Spearman's correlation coefficient. Many genes involved in the cholesterol or bile acid metabolism were highly correlated such as UDP-glucuronosyltransferase-21, apolipoprotein A-I and cMOAT. The mRNA content of the amyloid precursor protein (APP) showed the 5th highest correlation among the 8799 probes in the Affymetrix **Rat Genome U34** Array. In the livers of rats fed a high-cholesterol (1%) diet for 33 days, serum T.CHO levels increased by 4.6-fold, and the hepatic APP mRNA content also increased by 1.9-fold compared to the control group. These data suggest that the hepatic APP mRNA content was affected by serum T.CHO, and that hepatic APP was involved in cholesterol metabolism in rat livers.

L9 ANSWER 2 OF 16 CABA COPYRIGHT 2006 CABI on STN
ACCESSION NUMBER: 2004:119408 CABA
DOCUMENT NUMBER: 20043096244
TITLE: Effect of serum cholesterol on the mRNA content of amyloid precursor protein in rat livers
AUTHOR: Kiyosawa, N.; Ito, K.; Niino, N.; Sakuma, K.; Kanbori, M.; Yamoto, T.; Manabe, S.; Matsunuma, N.
CORPORATE SOURCE: Medicinal Safety Research Labs., Sankyo Co. Ltd., 717 Horikoshi, Fukuroi, Shizuoka 437-0065, Japan. kiyosawa@fuku.sankyo.co.jp
SOURCE: Toxicology Letters, (2004) Vol. 150, No. 2, pp. 157-166.
Publisher: Elsevier Science Ltd. Oxford
ISSN: 0378-4274
URL: http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6TCR-4BYC2VX-4&_user=10&_handle=B-WA-A-A-AW-MsSAYZW-UUA-AUEAUWVECC-AUYYZUCDCC-VEACVBDWA-AW-U&_fmt=summary&_coverDate=04%2F21%2F2004&_rdoc=3&_orig=browse&_srch=%23toc%235177%232004%23998499997%23496468!&_cdi=5177&view=c&_acct=C000050221&_version=1&_urlVersion=0&_userid=10&md5=2fca2bf1919a5db6bfaf224

c83ccb996
DOI: 10.1016/j.toxlet.2004.01.004
PUB. COUNTRY: United Kingdom
DOCUMENT TYPE: Journal
LANGUAGE: English
ENTRY DATE: Entered STN: 6 Aug 2004
Last Updated on STN: 6 Aug 2004

AB Genes that showed mRNA content profiles, which correlated with serum concentrations of total cholesterol (T.CHO), were screened from the microarray data of phenobarbital (PB)- or clofibrate (CLO)-treated rat livers, and the correlation was evaluated based on Spearman's correlation coefficient. Many genes involved in the cholesterol or bile acid metabolism were highly correlated such as UDP-glucuronosyltransferase-21, apolipoprotein A-I and cMOAT. The mRNA content of the amyloid precursor protein (APP) showed the 5th highest correlation among the 8799 probes in the Affymetrix **Rat Genome U34** Array. In the livers of rats fed a high-cholesterol (1%) diet for 33 days, serum T.CHO levels increased by 4.6-fold, and the hepatic APP mRNA content also increased by 1.9-fold compared to the control group. These data suggest that the hepatic APP mRNA content was affected by serum T.CHO, and that hepatic APP was involved in cholesterol metabolism in rat livers.

L9 ANSWER 3 OF 16 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:318664 CAPLUS
DOCUMENT NUMBER: 142:353091
TITLE: The RET/PTC-RAS-BRAF linear signaling cascade mediates the motile and mitogenic phenotype of thyroid cancer cells
AUTHOR(S): Melillo, Rosa Marina; Castellone, Maria Domenica; Guarino, Valentina; De Falco, Valentina; Cirafici, Anna Maria; Salvatore, Giuliana; Caiazzo, Fiorina; Basolo, Fulvio; Giannini, Riccardo; Kruhoffer, Mogens; Orntoft, Torben; Fusco, Alfredo; Santoro, Massimo
CORPORATE SOURCE: Istituto di Endocrinologia ed Oncologia Sperimentale del CNR "G. Salvatore," Dipartimento di Biologia e Patologia Cellulare e Molecolare, University "Federico II", Naples, Italy
SOURCE: Journal of Clinical Investigation (2005), 115(4), 1068-1081
CODEN: JCINAO; ISSN: 0021-9738
PUBLISHER: American Society for Clinical Investigation
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In papillary thyroid carcinomas (PTCs), rearrangements of the RET receptor (RET/PTC) and activating mutations in the BRAF or RAS oncogenes are mutually exclusive. Here the authors show that the 3 proteins function along a linear oncogenic signaling cascade in which RET/PTC induces RAS-dependent BRAF activation and RAS- and BRAF-dependent ERK activation. Adoptive activation of the RET/PTC-RAS-BRAF axis induced cell proliferation and Matrigel invasion of thyroid follicular cells. Gene expression profiling revealed that the 3 oncogenes activate a common transcriptional program in thyroid cells that includes upregulation of the CXCL1 and CXCL10 chemokines, which in turn stimulate proliferation and invasion. Thus, motile and mitogenic properties are intrinsic to transformed thyroid cells and are governed by an epistatic oncogenic signaling cascade.

REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 16 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:715674 CAPLUS
DOCUMENT NUMBER: 141:329675
TITLE: Differential expression of immunoregulatory genes in male and female Norway rats following infection with

Seoul virus
AUTHOR(S): Klein, Sabra L.; Cernetich, Amy; Hilmer, Sara; Hoffman, Eric P.; Scott, Alan L.; Glass, Gregory E.
CORPORATE SOURCE: W. Harry Feinstone Department of Molecular Microbiology and Immunology, The Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA
SOURCE: Journal of Medical Virology (2004), 74(1), 180-190
CODEN: JMVIDB; ISSN: 0146-6615
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Males of many species are more susceptible than females to infections caused by parasites, bacteria, fungi, and viruses. Following inoculation with Seoul virus, male rats have more virus present in target organs and shed virus longer than females. The goal of this study was to test the hypothesis that variation in the expression of genes associated with immune function mediates sex differences in hantavirus infection. Using DNA microarrays, the authors examined changes in gene expression in lung tissue during the early (when animals are viremic and shedding virus; Day 15 post-inoculation (p.i.)) and late (animals have low levels of infectious virus, but high antibody titers; Day 40 p.i.) phases of infection in adult male and female rats. After normalizing the gene expression levels from infected animals to the gene expression levels from same-sex uninfected controls, the data revealed that 1813 genes were differentially expressed between the sexes during infection. The expression of key transcriptional factors (e.g., eIF-2α, NF-κB, IRF-1, NF-IL-6, and STAT6) and genes that encode for proinflammatory (e.g., TNFαR, IL-1R, and IL-1RAcP), antiviral (e.g., IFNγR and Mx proteins), T cell (e.g., CD3 and TCR), and Ig superfamily (e.g., IgM, IgG, and MHC class I and II) proteins was higher in females than males. Conversely, males had higher expression of heat shock protein genes (e.g., hsp70) suggesting that cellular stress is elevated in males. These data provide candidate genes and cellular pathways that may underlie sex differences in responses to Seoul virus and possibly other hemorrhagic fever viruses.

REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 5 OF 16 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:319886 CAPLUS
DOCUMENT NUMBER: 141:20747
TITLE: Effect of serum cholesterol on the mRNA content of amyloid precursor protein in rat livers
AUTHOR(S): Kiyosawa, Naoki; Ito, Kazumi; Niino, Noriyo; Sakuma, Kyoko; Kanbori, Miyuki; Yamoto, Takashi; Manabe, Sunao; Matsunuma, Naochika
CORPORATE SOURCE: Medicinal Safety Research Labs., Sankyo Co. Ltd., Fukuroi, Shizuoka, 437-0065, Japan
SOURCE: Toxicology Letters (2004), 150(2), 157-166
CODEN: TOLED5; ISSN: 0378-4274
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Genes that showed mRNA content profiles which correlated with serum concns. of total cholesterol (T.CHO) were screened from microarray data of phenobarbital (PB)- or clofibrate (CLO)-treated rat livers, and the correlation was evaluated based on Spearman's correlation coefficient Many genes involved in cholesterol or bile acid metabolism were highly correlated such as UDP-glucuronosyltransferase-21, apolipoprotein A-I and cMOAT. The mRNA content of the amyloid precursor protein (APP) showed the 5th highest correlation among the 8799 probes in the Affymetrix **Rat Genome U34** Array. In the livers of rats fed a high-cholesterol (1%) diet for 33 days, serum T.CHO levels increased by 4.6-fold, and the hepatic APP mRNA content also increased by 1.9-fold compared to the control group. These data suggest that the hepatic APP

mRNA content was affected by serum T.CHO and that hepatic APP was involved in cholesterol metabolism in rat livers.
REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 6 OF 16 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:151792 CAPLUS
DOCUMENT NUMBER: 140:373080
TITLE: Gene expression profile and histopathology of experimental bronchopulmonary dysplasia induced by prolonged oxidative stress
AUTHOR(S): Wagenaar, Gerry T. M.; ter Horst, Simone A. J.; van Gastelen, Margot A.; Leijser, Lara M.; Mauad, Thais; van der Velden, Pieter A.; de Heer, Emile; Hiemstra, Pieter S.; Poorthuis, Ben J. H. M.; Walther, Frans J.
CORPORATE SOURCE: Division of Neonatology, Department of Pediatrics, Leiden University Medical Center, Leiden, Neth.
SOURCE: Free Radical Biology & Medicine (2004), 36(6), 782-801
CODEN: FRBMEH; ISSN: 0891-5849
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Oxidative stress is an important factor in the pathogenesis of bronchopulmonary dysplasia (BPD), a chronic lung disease of premature infants characterized by arrested alveolar and vascular development of the immature lung. The authors investigated differential gene expression with DNA microarray anal. in premature rat lungs exposed to prolonged hyperoxia during the saccular stage of development, which closely resembles the development of the lungs of premature infants receiving neonatal intensive care. Expression profiles were largely confirmed by real-time RT-PCR (27 genes) and in line with histopathol. and fibrin deposition studied by Western blotting. Oxidative stress affected a complex orchestra of genes involved in inflammation, coagulation, fibrinolysis, extracellular matrix turnover, cell cycle, signal transduction, and alveolar enlargement and explains, at least in part, the pathol. alterations that occur in lungs developing BPD. Exciting findings were the magnitude of fibrin deposition; the upregulation of chemokine-induced neutrophilic chemoattractant-1 (CINC-1), monocyte chemoattractant protein-1 (MCP-1), amphiregulin, plasminogen activator inhibitor-1 (PAI-1), secretory leukocyte proteinase inhibitor (SLPI), matrix metalloproteinase-12 (MMP12), p21, metallothionein, and heme oxygenase (HO); and the downregulation of fibroblast growth factor receptor-4 (FGFR4) and vascular endothelial growth factor (VEGF) receptor-2 (Flk-1). These findings are not only of fundamental importance in the understanding of the pathophysiol. of BPD, but also essential for the development of new therapeutic strategies.
REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 7 OF 16 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:283289 BIOSIS
DOCUMENT NUMBER: PREV200400282992
TITLE: Effect of serum cholesterol on the mRNA content of amyloid precursor protein in rat livers.
AUTHOR(S): Kiyosawa, Naoki [Reprint Author]; Ito, Kazumi; Niino, Noriyo; Sakuma, Kyoko; Kanbori, Miyuki; Yamoto, Takashi; Manabe, Sunao; Matsunuma, Naochika
CORPORATE SOURCE: Med Safety Res Labs, Sankyo Co Ltd, 717 Horikoshi, Shizuoka, 4370065, Japan
kiyosawa@fuku.sankyo.co.jp
SOURCE: Toxicology Letters (Shannon), (April 21 2004) Vol. 150, No. 2, pp. 157-166. print.
CODEN: TOLED5. ISSN: 0378-4274.
DOCUMENT TYPE: Article

LANGUAGE: English
ENTRY DATE: Entered STN: 9 Jun 2004
Last Updated on STN: 9 Jun 2004

AB Genes that showed mRNA content profiles, which correlated with serum concentrations of total cholesterol (T.CHO), were screened from the microarray data of phenobarbital (PB)- or clofibrate (CLO)-treated rat livers, and the correlation was evaluated based on Spearman's correlation coefficient. Many genes involved in the cholesterol or bile acid metabolism were highly correlated such as UDP-glucuronosyltransferase-21, apolipoprotein A-I and cMOAT. The mRNA content of the amyloid precursor protein (APP) showed the 5th highest correlation among the 8799 probes in the Affymetrix **Rat Genome U34** Array. In the livers of rats fed a high-cholesterol (1%) diet for 33 days, serum T.CHO levels increased by 4.6-fold, and the hepatic APP mRNA content also increased by 1.9-fold compared to the control group. These data suggest that the hepatic APP mRNA content was affected by serum T.CHO, and that hepatic APP was involved in cholesterol metabolism in rat livers.

L9 ANSWER 8 OF 16 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:197316 BIOSIS
DOCUMENT NUMBER: PREV200400197875
TITLE: Expression of structural genes in sensory ganglia of streptozotocin - diabetic rats by gene array profiling.
AUTHOR(S): Burnand, R. C. [Reprint Author]; McElhaney, M.; Barker, D.; Zhang, M.; Allendoerfer, K. L.; Dudek, H.; Rubin, L. L.; Tomlinson, D. R. [Reprint Author]
CORPORATE SOURCE: Neurosci., Univ. of Manchester, Manchester, UK
SOURCE: Society for Neuroscience Abstract Viewer and Itinerary Planner, (2003) Vol. 2003, pp. Abstract No. 311.13. http://sfn.scholarone.com. e-file.
Meeting Info.: 33rd Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 08-12, 2003. Society of Neuroscience.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 14 Apr 2004
Last Updated on STN: 14 Apr 2004

AB Hedgehog proteins are a family of morphogens with key roles in embryogenesis; effects in the adult are under explored. Treatment of STZ-diabetic rats with sonic hedgehog (Shh) reverses many indices of diabetic neuropathy by an unknown mechanism. Diabetic rats were treated with a sonic hedgehog-rat IgG fusion protein (Shh-IgG) and motor and sensory nerve conduction velocity (NCV) measured to verify a positive functional effect; both were normalised in the treated diabetic group. Reverse transcribed RNA from the L4 and L5 dorsal root ganglia (DRG) was hybridised to Affymetrix **Rat Genome U34** GeneChip"mu arrays. The results were scanned for the expression of genes that where altered in the diabetic model and brought back to the control trend with Shh-IgG treatment. Expression of the structural proteins: gamma actin, beta actin, alpha tubulin, NF-L, NF-M and NF-H was reduced in diabetes (36%, 52%, 35%, 32%, 33% and 21% respectively) and brought close to control levels with Shh-IgG treatment. Abnormalities in the synthesis of these proteins leads to an impairment of axonal structure and function. A restoration in the expression of these mRNAs provides us with a possible mechanism by which the deficit in NCV is reversed with hedgehog treatment.

L9 ANSWER 9 OF 16 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:193980 BIOSIS
DOCUMENT NUMBER: PREV200400194540
TITLE: Regulation of immune - related genes by neuronal activation.
AUTHOR(S): LaBuz, E. A. [Reprint Author]; McIntyre, D. C.; Herkenham,

M. [Reprint Author]; Foster, J. A. [Reprint Author]
CORPORATE SOURCE: Section on Functional NeuroAnat., NIMH Lab. Cell. and Molec Regulation, Bethesda, MD, USA
SOURCE: Society for Neuroscience Abstract Viewer and Itinerary Planner, (2003) Vol. 2003, pp. Abstract No. 103.20. http://sfn.scholarone.com. e-file.
Meeting Info.: 33rd Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 08-12, 2003. Society of Neuroscience.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 14 Apr 2004
Last Updated on STN: 14 Apr 2004

AB Many immune molecules and the genes encoding them have been recognized to be present in the CNS. Immune molecules in the brain contribute to the brain's response to peripheral and central infection and to the development of CNS autoimmune disease. In addition, immune molecule expression may be upregulated in the CNS in response to changes in neuronal activity not involving immune insults. In collaboration with Gene Logic, Inc., we performed a high-throughput assessment of gene expression using the Affymetrix Gene Chip **Rat Genome U34** set. The goal of this project was to identify activity-dependent changes in gene expression in rat hippocampus and prefrontal cortex following a single electroconvulsive shock (ECS). Analysis was performed using the proprietary GeneExpress software system to identify differentially expressed gene sequences. Several immune-related genes were upregulated including CD24, a cell surface glycoprotein that may play a role in neurogenesis; fractalkine, a neuronal expressed chemokine; and the tissue inhibitors of metalloproteinases (TIMPs) gene family, the endogenous inhibitors of matrix metalloproteinases (MMPs). Interestingly, we observed an increase in expression of several anti-inflammatory genes. In contrast, we did not observe an increase in pro-inflammatory genes. We believe that activation of such an anti-inflammatory "program" may be a neuroprotective response. Further studies, using the hippocampal kindling paradigm, are underway to examine whether activation of this anti-inflammatory program is a common feature of seizure.

L9 ANSWER 10 OF 16 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:515107 BIOSIS
DOCUMENT NUMBER: PREV200300512250
TITLE: MICROARRAY ANALYSIS OF GENES EXPRESSED IN A RAT MODEL OF ANTERIOR ISCHEMIC OPTIC NEUROPATHY.
AUTHOR(S): Emmert-Buck, L. T. [Reprint Author]; Mintz, M.; Stephan, D.; Bernstein, S. L. [Reprint Author]
CORPORATE SOURCE: Ophthalmology, University of Maryland, Baltimore, MD, USA
SOURCE: ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 624. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision and Ophthalmology.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 5 Nov 2003
Last Updated on STN: 5 Nov 2003

AB Purpose: We recently described a rat model of anterior ischemic optic neuropathy (AION). Here we describe the further gene expression analysis of the retina and optic nerve tissue extracted from the AION rat model. Methods: AION was photoembolically induced in animals using an argon laser

as previously described, via a custom-designed fundus contact lens. One eye was left untreated as a control. After induction, animals were sacrificed at 1 and 3 days. Retinae were harvested and retinal tissues immediately stored at -20degreeC. Total RNA was isolated from retina using The Qiaprep system (Qiagen Corp; Valencia, CA) per the manufacturer's directions. PolyA+ mRNA was subsequently isolated using Oligotex (Qiagen) per the manufacturer's directions. Initial messenger RNA quality was confirmed using denaturing formaldehyde gel electrophoresis. Hybridization probes were prepared using an Enzo BioArray High Yield RNA Transcript Labeling kit per the manufacturer's instructions. Probes were hybridized to a **Rat Genome U34** Set GeneChip Array (Affymetrix, Santa Clara, CA) per manufacturer's instructions. Results were analyzed using proprietary software (Affymetrix, Santa Clara, CA), and cluster analysis performed using the Genespring package. Results: Genes specific for ophthalmic and neural tissue are highly expressed in the rat retina RNA. There were significant shifts in specific genes that may be associated with AION induction. Cluster analysis has provided additional information regarding the specific categories of genes expressed. Alteration in specific gene patterns correlate in part with general retinal stress, as well as potential RGC-specific metabolic proteins that may be directly related to the retinal ganglion cell loss observed in previous studies. Conclusions: Analysis of the rat AION model continue to provide insight into the pathological basis of AION. We have shown that eye-specific and neuro-specific genes are highly expressed in the rat AION model when compared to controls and that the expression of these genes may be correlated with retinal ganglion cell loss. The expression of individual genes are being verified using additional techniques such as Northern analysis and rtPCR. The protein products of the identified genes may be potentially useful as therapeutic targets to treat or prevent AION.

L9 ANSWER 11 OF 16 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2003:325749 BIOSIS
DOCUMENT NUMBER: PREV200300325749
TITLE: GENE EXPRESSION PROFILING OF RAT ISCHEMIA, USING A GENECHIP STUDY.
AUTHOR(S): Tsuchiya, K. [Reprint Author]; Nishida, Y.; Sugahara, M. [Reprint Author]; Murata, A.; Nagata, T.; Takahashi, Y.; Ishikawa, K. [Reprint Author]; Asai, S.
CORPORATE SOURCE: pharmacology, nihon university school of medicine, tokyo, Japan
SOURCE: Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002) Vol. 2002, pp. Abstract No. 697.1. http://sfn.scholarone.com. cd-rom.
Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience. Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.
DOCUMENT TYPE: Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 16 Jul 2003
Last Updated on STN: 16 Jul 2003

AB To investigate the change in the distribution of EST mRNA expression in the brain during global cerebral ischemia and reperfusion, we used the **Rat Genome U34** Array (GeneChip, Affymetrix) to detect alterations in gene expression in the rat hippocampus subjected to 10 minutes of global cerebral ischemia followed by reperfusion for 2 h. We found at least a double increase in the expression of 122 genes after 2 h of reperfusion following ischemia. In this experiment, we selected one of the EST genes that at least doubled its expression after 2 h of reperfusion following ischemia. We used the probes to detect the specific EST mRNA in rat brain tissues by in situ hybridization which can identify

and localize the EST-gene expression at a single cell level. Our results indicated that the expression of EST gene was induced in several types of whole nervous system cells, including both neurons and nonneuronal cells in rat brain after 2 h of reperfusion following ischemia. We are presently investigating the full-length cDNA sequence of this EST gene and other genes with at least a 200% increase in their expression after 2 h of reperfusion following ischemia.

L9 ANSWER 12 OF 16 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2003:296584 BIOSIS
DOCUMENT NUMBER: PREV200300296584
TITLE: Gene expression profile of oxygen-induced bronchopulmonary dysplasia in a rat model.
AUTHOR(S): Wagenaar, Gerry T. [Reprint Author]; van Gastelen, Margot A.; Leijser, Lara M.; Mauad, Thais; De Heer, Emile; Hiemstra, Pieter S.; Poorthuis, Ben J.; Walther, Frans J.
CORPORATE SOURCE: Pediatrics, Leiden University Medical Center, Leiden, Netherlands
SOURCE: Pediatric Research, (April 2003) Vol. 53, No. 4 Part 2, pp. 413A. print.
Meeting Info.: Annual Meeting of the Pediatric Academic Societies. Seattle, WA, USA. May 03-06, 2003. Pediatric Academic Societies.
ISSN: 0031-3998 (ISSN print).
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 25 Jun 2003
Last Updated on STN: 25 Jun 2003

L9 ANSWER 13 OF 16 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2001:482583 BIOSIS
DOCUMENT NUMBER: PREV200100482583
TITLE: Gene profiling of PC12 cells treated with nerve growth factor.
AUTHOR(S): Langer-Gould, A. [Reprint author]; Garren, H. [Reprint author]; Steinman, L. [Reprint author]; Mobley, W. C. [Reprint author]
CORPORATE SOURCE: Neurology, Stanford University, Stanford, CA, USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1, pp. 357. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience. San Diego, California, USA. November 10-15, 2001.
ISSN: 0190-5295.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 17 Oct 2001
Last Updated on STN: 23 Feb 2002

AB Background: Nerve growth factor (NGF) treatment in vivo and in vitro, mediates neuronal survival, repair and differentiation in the central nervous system. PC12 cells serve as a useful model for studying NGF effects. Objective: To identify early-, intermediate and secondary changes in gene expression induced by NGF in PC12 cells that may account for NGF's ability to promote neuronal differentiation and survival. Methods: The pattern of gene expression in PC12 cells treated with NGF for 45 minutes, 3 hours, 24 hours and 1 week were examined using Affymetrix **Rat Genome U34** Arrays. Results were analyzed using Affymetrix software. Fold changes in gene expression were calculated at each time point using untreated PC12 cells as a baseline.

Results: NGF treatment of PC12 cells initially produces a proliferative response, followed by growth arrest and differentiation into a neuronal phenotype, all of which are reflected by our data. Of the 7000 known genes represented on arrays, over 600 were differentially expressed at at least one time point (fold change >2 or <0.5) in this experiment. Over half of these genes have never been reported to be induced or down-regulated by NGF; included in this list are genes known to be important in human diseases such as Alzheimer's disease, neuropathies, muscular dystrophy, leukemia and malignancies. Conclusion: Further study of the genes and their proteins gleaned from the candidate list may provide useful insight into the role of NGF in disease processes and their treatments.

L9 ANSWER 14 OF 16 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 2004333844 EMBASE
TITLE: Microarray platforms - Comparisons and contrasts.
AUTHOR: Hardiman G.
CORPORATE SOURCE: G. Hardiman, Biomed. Genomics Microarray Facility, Department of Medicine, University of California San Diego, La Jolla, CA 92093-0349, United States. ghardiman@ucsd.edu
SOURCE: Pharmacogenomics, (2004) Vol. 5, No. 5, pp. 487-502. .
Refs: 42
ISSN: 1462-2416 CODEN: PARMFL
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 022 Human Genetics
027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 19 Aug 2004
Last Updated on STN: 19 Aug 2004

AB In the relatively few years since their inception, DNA microarrays and Affymetrix GeneChips® have gained increasing use and acceptance in the study of genetic and cellular processes. This is evident from the rising number of published literature citing microarrays each year. With time, gene chips and microarrays have matured into complex technologies as biologists have teamed with applied mathematicians and statisticians to increase the rigor of experimentation and address the problems associated with the manipulation of large data sets. Several complementary microarray technologies for measuring gene expression are now routinely employed. This review will discuss the similarities and differences among these technologies and cover recent efforts to integrate data from cross-platform comparative studies. 2004 .COPYRGT. Future Medicine Ltd.

L9 ANSWER 15 OF 16 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 2004171316 EMBASE
TITLE: Effect of serum cholesterol on the mRNA content of amyloid precursor protein in rat livers.
AUTHOR: Kiyosawa N.; Ito K.; Niino N.; Sakuma K.; Kanbori M.; Yamoto T.; Manabe S.; Matsunuma N.
CORPORATE SOURCE: N. Kiyosawa, Medicinal Safety Research Labs., Sankyo Co. Ltd., 717 Horikoshi, Fukuroi, Shizuoka 437-0065, Japan. kiyosawa@fuku.sankyo.co.jp
SOURCE: Toxicology Letters, (21 Apr 2004) Vol. 150, No. 2, pp. 157-166. .
Refs: 35
ISSN: 0378-4274 CODEN: TOLED5
PUBLISHER IDENT.: S 0378-4274(04)00025-6
COUNTRY: Ireland
DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 022 Human Genetics
037 Drug Literature Index
052 Toxicology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 6 May 2004
Last Updated on STN: 6 May 2004

AB Genes that showed mRNA content profiles, which correlated with serum concentrations of total cholesterol (T.CHO), were screened from the microarray data of phenobarbital (PB)- or clofibrate (CLO)-treated rat livers, and the correlation was evaluated based on Spearman's correlation coefficient. Many genes involved in the cholesterol or bile acid metabolism were highly correlated such as UDP-glucuronosyltransferase-21, apolipoprotein A-I and cMOAT. The mRNA content of the amyloid precursor protein (APP) showed the 5th highest correlation among the 8799 probes in the Affymetrix **Rat Genome U34** Array. In the livers of rats fed a high-cholesterol (1%) diet for 33 days, serum T.CHO levels increased by 4.6-fold, and the hepatic APP mRNA content also increased by 1.9-fold compared to the control group. These data suggest that the hepatic APP mRNA content was affected by serum T.CHO, and that hepatic APP was involved in cholesterol metabolism in rat livers.

L9 ANSWER 16 OF 16 EMBASE
ACCESSION NUMBER: 2002240694 EMBASE
TITLE: Etiology-specific gene expression profiles in rat mammary carcinomas.
AUTHOR: Kuramoto T.; Morimura K.; Yamashita S.; Okochi E.; Watanabe N.; Ohta T.; Ohki M.; Fukushima S.; Sugimura T.; Ushijima T.
CORPORATE SOURCE: T. Ushijima, Carcinogenesis Division, Natl. Cancer Ctr. Research Institute, 5-1-1 Tsukiji, Chuo-ku, Tokyo 104-0045, Japan. tushijim@ncc.go.jp
SOURCE: Cancer Research, (1 Jul 2002) Vol. 62, No. 13, pp. 3592-3597. .
Refs: 39
ISSN: 0008-5472 CODEN: CNREA8
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
022 Human Genetics
027 Biophysics, Bioengineering and Medical Instrumentation
052 Toxicology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 25 Jul 2002
Last Updated on STN: 25 Jul 2002

AB Identification of etiology of human cancers is important for effective cancer prevention, and attempts to estimate the roles of a variety of environmental carcinogens in human cancers are being made. Here, we applied cDNA microarray technology to estimate whether gene expression profiles of cancers would reflect their etiology. Using rat mammary carcinoma models, expression profiles were analyzed in two groups of carcinomas induced by distinct carcinogens but with the same histological classification. Four carcinomas induced by 7,12-dimethylbenz[a]anthracene (DMBA) and three carcinomas induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine (PhIP) and a high-fat diet were analyzed by a GeneChip oligonucleotide microarray that contained .apprx.8000 rat genes. By hierarchical clustering analysis, the seven carcinomas were classified into two groups that exactly coincided with the DMBA-induced and the PhIP-induced groups. The correlation coefficient between the two groups was 0.63, and those between any carcinomas within each group ranged from

0.78 to 0.95. In addition, characteristic clusters of genes were also identified that highlighted distinct and common characteristics of both groups. Seventeen genes were down-regulated in the DMBA and upregulated in the PhIP-induced groups. Thirty-three genes were regulated in the opposite manner. Our results indicated that gene expression profiles in cancers reflect their etiology and suggested a possibility that etiology of cancers could be retrospectively estimated from their expression profiles.

=> dup rem l9
PROCESSING COMPLETED FOR L9
L10 12 DUP REM L9 (4 DUPLICATES REMOVED)

=> d l0 1- ibib abs
'L0' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files. Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):ibib abs
YOU HAVE REQUESTED DATA FROM 12 ANSWERS - CONTINUE? Y/(N):n

=> d l10 1- ibib abs
YOU HAVE REQUESTED DATA FROM 12 ANSWERS - CONTINUE? Y/(N):y

L10 ANSWER 1 OF 12 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:318664 CAPLUS
DOCUMENT NUMBER: 142:353091
TITLE: The RET/PTC-RAS-BRAF linear signaling cascade mediates the motile and mitogenic phenotype of thyroid cancer cells
AUTHOR(S): Melillo, Rosa Marina; Castellone, Maria Domenica; Guarino, Valentina; De Falco, Valentina; Cirafici, Anna Maria; Salvatore, Giuliana; Caiazzo, Fiorina; Basolo, Fulvio; Giannini, Riccardo; Kruhoffer, Mogens; Orntoft, Torben; Fusco, Alfredo; Santoro, Massimo
CORPORATE SOURCE: Istituto di Endocrinologia ed Oncologia Sperimentale del CNR "G. Salvatore," Dipartimento di Biologia e Patologia Cellulare e Molecolare, University "Federico II", Naples, Italy
SOURCE: Journal of Clinical Investigation (2005), 115(4), 1068-1081
CODEN: JCINAO; ISSN: 0021-9738
PUBLISHER: American Society for Clinical Investigation
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In papillary thyroid carcinomas (PTCs), rearrangements of the RET receptor (RET/PTC) and activating mutations in the BRAF or RAS oncogenes are mutually exclusive. Here the authors show that the 3 proteins function along a linear oncogenic signaling cascade in which RET/PTC induces RAS-dependent BRAF activation and RAS- and BRAF-dependent ERK activation. Adoptive activation of the RET/PTC-RAS-BRAF axis induced cell proliferation and Matrigel invasion of thyroid follicular cells. Gene expression profiling revealed that the 3 oncogenes activate a common transcriptional program in thyroid cells that includes upregulation of the CXCL1 and CXCL10 chemokines, which in turn stimulate proliferation and invasion. Thus, motile and mitogenic properties are intrinsic to transformed thyroid cells and are governed by an epistatic oncogenic signaling cascade.
REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 2 OF 12 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:151792 CAPLUS
DOCUMENT NUMBER: 140:373080
TITLE: Gene expression profile and histopathology of experimental bronchopulmonary dysplasia induced by prolonged oxidative stress
AUTHOR(S): Wagenaar, Gerry T. M.; ter Horst, Simone A. J.; van Gastelen, Margot A.; Leijser, Lara M.; Mauad, Thais; van der Velden, Pieter A.; de Heer, Emile; Hiemstra, Pieter S.; Poorthuis, Ben J. H. M.; Walther, Frans J.
CORPORATE SOURCE: Division of Neonatology, Department of Pediatrics, Leiden University Medical Center, Leiden, Neth.
SOURCE: Free Radical Biology & Medicine (2004), 36(6), 782-801
CODEN: FRBMEH; ISSN: 0891-5849
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Oxidative stress is an important factor in the pathogenesis of bronchopulmonary dysplasia (BPD), a chronic lung disease of premature infants characterized by arrested alveolar and vascular development of the immature lung. The authors investigated differential gene expression with DNA microarray anal. in premature rat lungs exposed to prolonged hyperoxia during the saccular stage of development, which closely resembles the development of the lungs of premature infants receiving neonatal intensive care. Expression profiles were largely confirmed by real-time RT-PCR (27 genes) and in line with histopathol. and fibrin deposition studied by Western blotting. Oxidative stress affected a complex orchestra of genes involved in inflammation, coagulation, fibrinolysis, extracellular matrix turnover, cell cycle, signal transduction, and alveolar enlargement and explains, at least in part, the pathol. alterations that occur in lungs developing BPD. Exciting findings were the magnitude of fibrin deposition; the upregulation of chemokine-induced neutrophilic chemoattractant-1 (CINC-1), monocyte chemoattractant protein-1 (MCP-1), amphiregulin, plasminogen activator inhibitor-1 (PAI-1), secretory leukocyte proteinase inhibitor (SLPI), matrix metalloproteinase-12 (MMP12), p21, metallothionein, and heme oxygenase (HO); and the downregulation of fibroblast growth factor receptor-4 (FGFR4) and vascular endothelial growth factor (VEGF) receptor-2 (Flk-1). These findings are not only of fundamental importance in the understanding of the pathophysiol. of BPD, but also essential for the development of new therapeutic strategies.
REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 3 OF 12 EMBASE
ACCESSION NUMBER: 2004333844 EMBASE
TITLE: Microarray platforms - Comparisons and contrasts.
AUTHOR: Hardiman G.
CORPORATE SOURCE: G. Hardiman, Biomed. Genomics Microarray Facility, Department of Medicine, University of California San Diego, La Jolla, CA 92093-0349, United States. ghardiman@ucsd.edu
SOURCE: Pharmacogenomics, (2004) Vol. 5, No. 5, pp. 487-502. .
Refs: 42
ISSN: 1462-2416 CODEN: PARMFL
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 022 Human Genetics
027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 19 Aug 2004
Last Updated on STN: 19 Aug 2004

AB In the relatively few years since their inception, DNA microarrays and Affymetrix GeneChips® have gained increasing use and acceptance in the study of genetic and cellular processes. This is evident from the rising number of published literature citing microarrays each year. With time, gene chips and microarrays have matured into complex technologies as biologists have teamed with applied mathematicians and statisticians to increase the rigor of experimentation and address the problems associated with the manipulation of large data sets. Several complementary microarray technologies for measuring gene expression are now routinely employed. This review will discuss the similarities and differences among these technologies and cover recent efforts to integrate data from cross-platform comparative studies. 2004 .COPYRGT. Future Medicine Ltd.

L10 ANSWER 4 OF 12 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:715674 CAPLUS
DOCUMENT NUMBER: 141:329675
TITLE: Differential expression of immunoregulatory genes in male and female Norway rats following infection with Seoul virus
AUTHOR(S): Klein, Sabra L.; Cernetich, Amy; Hilmer, Sara; Hoffman, Eric P.; Scott, Alan L.; Glass, Gregory E.
CORPORATE SOURCE: W. Harry Feinstone Department of Molecular Microbiology and Immunology, The Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA
SOURCE: Journal of Medical Virology (2004), 74(1), 180-190
CODEN: JMVIDB; ISSN: 0146-6615
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Males of many species are more susceptible than females to infections caused by parasites, bacteria, fungi, and viruses. Following inoculation with Seoul virus, male rats have more virus present in target organs and shed virus longer than females. The goal of this study was to test the hypothesis that variation in the expression of genes associated with immune function mediates sex differences in hantavirus infection. Using DNA microarrays, the authors examined changes in gene expression in lung tissue during the early (when animals are viremic and shedding virus; Day 15 post-inoculation (p.i.)) and late (animals have low levels of infectious virus, but high antibody titers; Day 40 p.i.) phases of infection in adult male and female rats. After normalizing the gene expression levels from infected animals to the gene expression levels from same-sex uninfected controls, the data revealed that 1813 genes were differentially expressed between the sexes during infection. The expression of key transcriptional factors (e.g., eIF-2α, NF-κB, IRF-1, NF-IL-6, and STAT6) and genes that encode for proinflammatory (e.g., TNFαR, IL-1R, and IL-1RAcP), antiviral (e.g., IFNγR and Mx proteins), T cell (e.g., CD3 and TCR), and Ig superfamily (e.g., IgM, IgG, and MHC class I and II) proteins was higher in females than males. Conversely, males had higher expression of heat shock protein genes (e.g., hsp70) suggesting that cellular stress is elevated in males. These data provide candidate genes and cellular pathways that may underlie sex differences in responses to Seoul virus and possibly other hemorrhagic fever viruses.
REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 5 OF 12 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2004198669 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15093671
TITLE: Effect of serum cholesterol on the mRNA content of amyloid precursor protein in rat livers.
AUTHOR: Kiyosawa Naoki; Ito Kazumi; Niino Noriyo; Sakuma Kyoko; Kanbori Miyuki; Yamoto Takashi; Manabe Sunao; Matsunuma Naochika
CORPORATE SOURCE: Medicinal Safety Research Labs., Sankyo Co. Ltd., 717

Horikoshi, Fukuroi, Shizuoka 437-0065, Japan..
kiyosawa@fuku.sankyo.co.jp
SOURCE: Toxicology letters, (2004 Apr 21) Vol. 150, No. 2, pp. 157-66.
Journal code: 7709027. ISSN: 0378-4274.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200405
ENTRY DATE: Entered STN: 20040420
Last Updated on STN: 20040521
Entered Medline: 20040520

AB Genes that showed mRNA content profiles, which correlated with serum concentrations of total cholesterol (T.CHO), were screened from the microarray data of phenobarbital (PB)- or clofibrate (CLO)-treated rat livers, and the correlation was evaluated based on Spearman's correlation coefficient. Many genes involved in the cholesterol or bile acid metabolism were highly correlated such as UDP-glucuronosyltransferase-21, apolipoprotein A-I and cMOAT. The mRNA content of the amyloid precursor protein (APP) showed the 5th highest correlation among the 8799 probes in the Affymetrix **Rat Genome U34** Array. In the
livers of rats fed a high-cholesterol (1%) diet for 33 days, serum T.CHO levels increased by 4.6-fold, and the hepatic APP mRNA content also increased by 1.9-fold compared to the control group. These data suggest that the hepatic APP mRNA content was affected by serum T.CHO, and that hepatic APP was involved in cholesterol metabolism in rat livers.

L10 ANSWER 6 OF 12 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:296584 BIOSIS
DOCUMENT NUMBER: PREV200300296584
TITLE: Gene expression profile of oxygen-induced bronchopulmonary dysplasia in a rat model.
AUTHOR(S): Wagenaar, Gerry T. [Reprint Author]; van Gastelen, Margot A.; Leijser, Lara M.; Mauad, Thais; De Heer, Emile; Hiemstra, Pieter S.; Poorthuis, Ben J.; Walther, Frans J.
CORPORATE SOURCE: Pediatrics, Leiden University Medical Center, Leiden, Netherlands
SOURCE: Pediatric Research, (April 2003) Vol. 53, No. 4 Part 2, pp. 413A. print.
Meeting Info.: Annual Meeting of the Pediatric Academic Societies. Seattle, WA, USA. May 03-06, 2003. Pediatric Academic Societies.
ISSN: 0031-3998 (ISSN print).
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 25 Jun 2003
Last Updated on STN: 25 Jun 2003

L10 ANSWER 7 OF 12 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:515107 BIOSIS
DOCUMENT NUMBER: PREV200300512250
TITLE: MICROARRAY ANALYSIS OF GENES EXPRESSED IN A RAT MODEL OF ANTERIOR ISCHEMIC OPTIC NEUROPATHY.
AUTHOR(S): Emmert-Buck, L. T. [Reprint Author]; Mintz, M.; Stephan, D.; Bernstein, S. L. [Reprint Author]
CORPORATE SOURCE: Ophthalmology, University of Maryland, Baltimore, MD, USA
SOURCE: ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 624. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision

and Ophthalmology.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 5 Nov 2003
Last Updated on STN: 5 Nov 2003

AB Purpose: We recently described a rat model of anterior ischemic optic neuropathy (AION). Here we describe the further gene expression analysis of the retina and optic nerve tissue extracted from the AION rat model. Methods: AION was photoembolically induced in animals using an argon laser as previously described, via a custom-designed fundus contact lens. One eye was left untreated as a control. After induction, animals were sacrificed at 1 and 3 days. Retinae were harvested and retinal tissues immediately stored at -20degreeC. Total RNA was isolated from retina using The Qiaprep system (Qiagen Corp; Valencia, CA) per the manufacturer's directions. PolyA+ mRNA was subsequently isolated using Oligotex (Qiagen) per the manufacturer's directions. Initial messenger RNA quality was confirmed using denaturing formaldehyde gel electrophoresis. Hybridization probes were prepared using an Enzo BioArray High Yield RNA Transcript Labeling kit per the manufacturer's instructions. Probes were hybridized to a **Rat Genome U34** Set GeneChip Array (Affymetrix, Santa Clara, CA) per manufacturer's instructions. Results were analyzed using proprietary software (Affymetrix, Santa Clara, CA), and cluster analysis performed using the Genespring package. Results: Genes specific for ophthalmic and neural tissue are highly expressed in the rat retina RNA. There were significant shifts in specific genes that may be associated with AION induction. Cluster analysis has provided additional information regarding the specific categories of genes expressed. Alteration in specific gene patterns correlate in part with general retinal stress, as well as potential RGC-specific metabolic proteins that may be directly related to the retinal ganglion cell loss observed in previous studies. Conclusions: Analysis of the rat AION model continue to provide insight into the pathological basis of AION. We have shown that eye-specific and neuro-specific genes are highly expressed in the rat AION model when compared to controls and that the expression of these genes may be correlated with retinal ganglion cell loss. The expression of individual genes are being verified using additional techniques such as Northern analysis and rtPCR. The protein products of the identified genes may be potentially useful as therapeutic targets to treat or prevent AION.

L10. ANSWER 8 OF 12 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:197316 BIOSIS
DOCUMENT NUMBER: PREV200400197875
TITLE: Expression of structural genes in sensory ganglia of streptozotocin - diabetic rats by gene array profiling.
AUTHOR(S): Burnand, R. C. [Reprint Author]; McElhaney, M.; Barker, D.; Zhang, M.; Allendoerfer, K. L.; Dudek, H.; Rubin, L. L.; Tomlinson, D. R. [Reprint Author]
CORPORATE SOURCE: Neurosci., Univ. of Manchester, Manchester, UK
SOURCE: Society for Neuroscience Abstract Viewer and Itinerary Planner, (2003) Vol. 2003, pp. Abstract No. 311.13. http://sfn.scholarone.com. e-file.
Meeting Info.: 33rd Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 08-12, 2003. Society of Neuroscience.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 14 Apr 2004
Last Updated on STN: 14 Apr 2004

AB Hedgehog proteins are a family of morphogens with key roles in embryogenesis; effects in the adult are under explored. Treatment of

STZ-diabetic rats with sonic hedgehog (Shh) reverses many indices of diabetic neuropathy by an unknown mechanism. Diabetic rats were treated with a sonic hedgehog-rat IgG fusion protein (Shh-IgG) and motor and sensory nerve conduction velocity (NCV) measured to verify a positive functional effect; both were normalised in the treated diabetic group. Reverse transcribed RNA from the L4 and L5 dorsal root ganglia (DRG) was hybridised to Affymetrix **Rat Genome U34** GeneChip"mu arrays. The results were scanned for the expression of genes that where altered in the diabetic model and brought back to the control trend with Shh-IgG treatment. Expression of the structural proteins: gamma actin, beta actin, alpha tubulin, NF-L, NF-M and NF-H was reduced in diabetes (36%, 52%, 35%, 32%, 33% and 21% respectively) and brought close to control levels with Shh-IgG treatment. Abnormalities in the synthesis of these proteins leads to an impairment of axonal structure and function. A restoration in the expression of these mRNAs provides us with a possible mechanism by which the deficit in NCV is reversed with hedgehog treatment.

L10 ANSWER 9 OF 12 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2004:193980 BIOSIS
DOCUMENT NUMBER: PREV200400194540
TITLE: Regulation of immune - related genes by neuronal activation.
AUTHOR(S): LaBuz, E. A. [Reprint Author]; McIntyre, D. C.; Herkenham, M. [Reprint Author]; Foster, J. A. [Reprint Author]
CORPORATE SOURCE: Section on Functional NeuroAnat., NIMH Lab. Cell. and Molec Regulation, Bethesda, MD, USA
SOURCE: Society for Neuroscience Abstract Viewer and Itinerary Planner, (2003) Vol. 2003, pp. Abstract No. 103.20. http://sfn.scholarone.com. e-file.
Meeting Info.: 33rd Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 08-12, 2003. Society of Neuroscience.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 14 Apr 2004
Last Updated on STN: 14 Apr 2004

AB Many immune molecules and the genes encoding them have been recognized to be present in the CNS. Immune molecules in the brain contribute to the brain's response to peripheral and central infection and to the development of CNS autoimmune disease. In addition, immune molecule expression may be upregulated in the CNS in response to changes in neuronal activity not involving immune insults. In collaboration with Gene Logic, Inc., we performed a high-throughput assessment of gene expression using the Affymetrix Gene Chip **Rat Genome U34** set. The goal of this project was to identify activity-dependent changes in gene expression in rat hippocampus and prefrontal cortex following a single electroconvulsive shock (ECS). Analysis was performed using the proprietary GeneExpress software system to identify differentially expressed gene sequences. Several immune-related genes were upregulated including CD24, a cell surface glycoprotein that may play a role in neurogenesis; fractalkine, a neuronal expressed chemokine; and the tissue inhibitors of metalloproteinases (TIMPs) gene family, the endogenous inhibitors of matrix metalloproteinases (MMPs). Interestingly, we observed an increase in expression of several anti-inflammatory genes. In contrast, we did not observe an increase in pro-inflammatory genes. We believe that activation of such an anti-inflammatory "program" may be a neuroprotective response. Further studies, using the hippocampal kindling paradigm, are underway to examine whether activation of this anti-inflammatory program is a common feature of seizure.

L10 ANSWER 10 OF 12 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 2002240694 EMBASE
TITLE: Etiology-specific gene expression profiles in rat mammary carcinomas.
AUTHOR: Kuramoto T.; Morimura K.; Yamashita S.; Okochi E.; Watanabe N.; Ohta T.; Ohki M.; Fukushima S.; Sugimura T.; Ushijima T.
CORPORATE SOURCE: T. Ushijima, Carcinogenesis Division, Natl. Cancer Ctr. Research Institute, 5-1-1 Tsukiji, Chuo-ku, Tokyo 104-0045, Japan. tushijim@ncc.go.jp
SOURCE: Cancer Research, (1 Jul 2002) Vol. 62, No. 13, pp. 3592-3597. .
Refs: 39
ISSN: 0008-5472 CODEN: CNREA8
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
022 Human Genetics
027 Biophysics, Bioengineering and Medical Instrumentation
052 Toxicology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 25 Jul 2002
Last Updated on STN: 25 Jul 2002

AB Identification of etiology of human cancers is important for effective cancer prevention, and attempts to estimate the roles of a variety of environmental carcinogens in human cancers are being made. Here, we applied cDNA microarray technology to estimate whether gene expression profiles of cancers would reflect their etiology. Using rat mammary carcinoma models, expression profiles were analyzed in two groups of carcinomas induced by distinct carcinogens but with the same histological classification. Four carcinomas induced by 7,12-dimethylbenz[a]anthracene (DMBA) and three carcinomas induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine (PhIP) and a high-fat diet were analyzed by a GeneChip oligonucleotide microarray that contained .apprx.8000 rat genes. By hierarchical clustering analysis, the seven carcinomas were classified into two groups that exactly coincided with the DMBA-induced and the PhIP-induced groups. The correlation coefficient between the two groups was 0.63, and those between any carcinomas within each group ranged from 0.78 to 0.95. In addition, characteristic clusters of genes were also identified that highlighted distinct and common characteristics of both groups. Seventeen genes were down-regulated in the DMBA and upregulated in the PhIP-induced groups. Thirty-three genes were regulated in the opposite manner. Our results indicated that gene expression profiles in cancers reflect their etiology and suggested a possibility that etiology of cancers could be retrospectively estimated from their expression profiles.

L10 ANSWER 11 OF 12 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:325749 BIOSIS
DOCUMENT NUMBER: PREV200300325749
TITLE: GENE EXPRESSION PROFILING OF RAT ISCHEMIA, USING A GENECHIP STUDY.
AUTHOR(S): Tsuchiya, K. [Reprint Author]; Nishida, Y.; Sugahara, M. [Reprint Author]; Murata, A.; Nagata, T.; Takahashi, Y.; Ishikawa, K. [Reprint Author]; Asai, S.
CORPORATE SOURCE: pharmacology, nihon university school of medicine, tokyo, Japan
SOURCE: Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002) Vol. 2002, pp. Abstract No. 697.1. http://sfn.scholarone.com. cd-rom.
Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience. Orlando, Florida, USA. November 02-07, 2002.

Society for Neuroscience.
DOCUMENT TYPE: Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 16 Jul 2003
Last Updated on STN: 16 Jul 2003

AB To investigate the change in the distribution of EST mRNA expression in the brain during global cerebral ischemia and reperfusion, we used the **Rat Genome U34** Array (GeneChip, Affymetrix) to detect alterations in gene expression in the rat hippocampus subjected to 10 minutes of global cerebral ischemia followed by reperfusion for 2 h. We found at least a double increase in the expression of 122 genes after 2 h of reperfusion following ischemia. In this experiment, we selected one of the EST genes that at least doubled its expression after 2 h of reperfusion following ischemia. We used the probes to detect the specific EST mRNA in rat brain tissues by in situ hybridization which can identify and localize the EST-gene expression at a single cell level. Our results indicated that the expression of EST gene was induced in several types of whole nervous system cells, including both neurons and nonneuronal cells in rat brain after 2 h of reperfusion following ischemia. We are presently investigating the full-length cDNA sequence of this EST gene and other genes with at least a 200% increase in their expression after 2 h of reperfusion following ischemia.

L10 ANSWER 12 OF 12 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2001:482583 BIOSIS
DOCUMENT NUMBER: PREV200100482583
TITLE: Gene profiling of PC12 cells treated with nerve growth factor.
AUTHOR(S): Langer-Gould, A. [Reprint author]; Garren, H. [Reprint author]; Steinman, L. [Reprint author]; Mobley, W. C. [Reprint author]
CORPORATE SOURCE: Neurology, Stanford University, Stanford, CA, USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1, pp. 357. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience. San Diego, California, USA. November 10-15, 2001.
ISSN: 0190-5295.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 17 Oct 2001
Last Updated on STN: 23 Feb 2002

AB Background: Nerve growth factor (NGF) treatment in vivo and in vitro, mediates neuronal survival, repair and differentiation in the central nervous system. PC12 cells serve as a useful model for studying NGF effects. Objective: To identify early-, intermediate and secondary changes in gene expression induced by NGF in PC12 cells that may account for NGF's ability to promote neuronal differentiation and survival. Methods: The pattern of gene expression in PC12 cells treated with NGF for 45 minutes, 3 hours, 24 hours and 1 week were examined using Affymetrix **Rat Genome U34** Arrays. Results were analyzed using Affymetrix software. Fold changes in gene expression were calculated at each time point using untreated PC12 cells as a baseline. Results: NGF treatment of PC12 cells initially produces a proliferative response, followed by growth arrest and differentiation into a neuronal phenotype, all of which are reflected by our data. Of the 7000 known genes represented on arrays, over 600 were differentially expressed at at least one time point (fold change >2 or <0.5) in this experiment. Over half of these genes have never been reported to be induced or down-regulated by NGF; included in this list are genes known to be

important in human diseases such as Alzheimer's disease, neuropathies, muscular dystrophy, leukemia and malignancies. Conclusion: Further study of the genes and their proteins gleaned from the candidate list may provide useful insight into the role of NGF in disease processes and their treatments.

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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
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=> codelink rat whole
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             1 RAT
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L11          0 CODELINK RAT WHOLE
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=> file .cluster1
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
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FULL ESTIMATED COST                                     0.48     118.37

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CA SUBSCRIBER PRICE                                     0.00      -5.25

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=> codelink rat whole
L12          0 CODELINK RAT WHOLE
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=> rat whole genome
L13 6 RAT WHOLE GENOME

=> d l13 1i ibib abs
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REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):d l13 1- ibib abs
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REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):ibib abs

L13 ANSWER 1 OF 6 MEDLINE on STN
ACCESSION NUMBER: 2003271783 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12798933
TITLE: Genomic evidence for the absence of a functional cholesteryl ester transfer protein gene in mice and rats.
AUTHOR: Hogarth Cathryn A; Roy Alison; Ebert David L
CORPORATE SOURCE: Russell Grimwade School of Biochemistry and Molecular Biology, University of Melbourne, Parkville, Victoria 3010, Australia.
SOURCE: Comparative biochemistry and physiology. Part B, Biochemistry & molecular biology, (2003 Jun) Vol. 135, No. 2, pp. 219-29.
Journal code: 9516061. ISSN: 1096-4959.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200403
ENTRY DATE: Entered STN: 20030612
Last Updated on STN: 20040324
Entered Medline: 20040323
AB Mice and rats are naturally deficient in cholesteryl ester transfer protein (CETP) activity, although the reason behind the deficiency in activity is unknown. A search of mouse genome databases revealed sequences resembling 7 of the 16 human exons. However, these sequences could not code for a functional CETP. Analysis of the rat genome using Southern blotting revealed sequences complementary to human CETP cDNA, but RNase protection assays were unable to detect any Cetp gene expression in liver, adipose, or muscle. A search of **rat whole-genome** shotgun databases revealed exon-like sequences that would be unable to code for a functional CETP. An Ap3s1 pseudogene lay immediately upstream of the CETP-like sequences in mouse, but was nearly identical to the functional gene and unlikely to have been inserted prior to mouse-rat divergence. In contrast, a deletion leading to a nonsense codon was found in the exon 11-like sequences of both rat and mouse and not in any other species. Thus, the lack of CETP activity in both the mouse and the rat is most likely due to an evolutionary event that occurred before these species diverged and not to altered regulation of the gene or function of the gene product.

=> d l13 1- ibib abs
YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):y

L13 ANSWER 1 OF 6 MEDLINE on STN
ACCESSION NUMBER: 2003271783 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12798933

TITLE: Genomic evidence for the absence of a functional cholesteryl ester transfer protein gene in mice and rats.
AUTHOR: Hogarth Cathryn A; Roy Alison; Ebert David L
CORPORATE SOURCE: Russell Grimwade School of Biochemistry and Molecular Biology, University of Melbourne, Parkville, Victoria 3010, Australia.
SOURCE: Comparative biochemistry and physiology. Part B, Biochemistry & molecular biology, (2003 Jun) Vol. 135, No. 2, pp. 219-29.
Journal code: 9516061. ISSN: 1096-4959.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200403
ENTRY DATE: Entered STN: 20030612
Last Updated on STN: 20040324
Entered Medline: 20040323

AB Mice and rats are naturally deficient in cholesteryl ester transfer protein (CETP) activity, although the reason behind the deficiency in activity is unknown. A search of mouse genome databases revealed sequences resembling 7 of the 16 human exons. However, these sequences could not code for a functional CETP. Analysis of the rat genome using Southern blotting revealed sequences complementary to human CETP cDNA, but RNase protection assays were unable to detect any Cetp gene expression in liver, adipose, or muscle. A search of **rat whole-genome** shotgun databases revealed exon-like sequences that would be unable to code for a functional CETP. An Ap3s1 pseudogene lay immediately upstream of the CETP-like sequences in mouse, but was nearly identical to the functional gene and unlikely to have been inserted prior to mouse-rat divergence. In contrast, a deletion leading to a nonsense codon was found in the exon 11-like sequences of both rat and mouse and not in any other species. Thus, the lack of CETP activity in both the mouse and the rat is most likely due to an evolutionary event that occurred before these species diverged and not to altered regulation of the gene or function of the gene product.

L13 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:442584 CAPLUS
DOCUMENT NUMBER: 139:192246
TITLE: Genomic evidence for the absence of a functional cholesteryl ester transfer protein gene in mice and rats
AUTHOR(S): Hogarth, Cathryn A.; Roy, Alison; Ebert, David L.
CORPORATE SOURCE: Russell Grimwade School of Biochemistry and Molecular Biology, University of Melbourne, Victoria, 3010, Australia
SOURCE: Comparative Biochemistry and Physiology, Part B: Biochemistry & Molecular Biology (2003), 135B(2), 219-229
CODEN: CBPBB8; ISSN: 1096-4959
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Mice and rats are naturally deficient in cholesteryl ester transfer protein (CETP) activity, although the reason behind the deficiency in activity is unknown. A search of mouse genome databases revealed sequences resembling 7 of the 16 human exons. However, these sequences could not code for a functional CETP. Anal. of the rat genome using Southern blotting revealed sequences complementary to human CETP cDNA, but RNase protection assays were unable to detect any Cetp gene expression in liver, adipose, or muscle. A search of **rat whole-genome** shotgun databases revealed exon-like sequences that would be unable to code for a functional CETP. An Ap3s1 pseudogene lay

immediately upstream of the CETP-like sequences in mouse, but was nearly identical to the functional gene and unlikely to have been inserted prior to mouse-rat divergence. In contrast, a deletion leading to a nonsense codon was found in the exon 11-like sequences of both rat and mouse and not in any other species. Thus, the lack of CETP activity in both the mouse and the rat is most likely due to an evolutionary event that occurred before these species diverged and not to altered regulation of the gene or function of the gene product.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2000:727692 CAPLUS
DOCUMENT NUMBER: 135:29661
TITLE: A whole-genome radiation hybrid panel and framework map of the rat genome
AUTHOR(S): McCarthy, Linda C.; Bihoreau, Marie-Therese; Kiguwa, Susanna L.; Browne, Julie; Watanabe, Takeshi K.; Hishigaki, Haretsugu; Tsuji, Atsushi; Kiel, Susanne; Webber, Caleb; Davis, Maria E.; Knights, Catherine; Smith, Angela; Critcher, Ricky; Huxtall, Patrick; Hudson, James R., Jr.; Ono, Toshihide; Hayashi, Hiroumi; Takagi, Toshihisa; Nakamura, Yusuke; Tanigami, Akira; Goodfellow, Peter N.; Lathrop, G. Mark; James, Michael R.
CORPORATE SOURCE: Department of Genetics, University of Cambridge, Cambridge, CB2 3EH, UK
SOURCE: Mammalian Genome (2000), 11(9), 791-795
CODEN: MAMGEC; ISSN: 0938-8990
PUBLISHER: Springer-Verlag New York Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Rat genome-wide maps based on the T55 radiation hybrid (RH) panel have previously been presented. Here, the authors characterize this panel in detail and describe the optimal subset of RHs with which a genome-wide framework map have been constructed, which makes this resource immediately useful to everyone involved in genetic studies with rat.
REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 4 OF 6 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:374931 BIOSIS
DOCUMENT NUMBER: PREV200300374931
TITLE: Genomic evidence for the absence of a functional cholesteryl ester transfer protein gene in mice and rats.
AUTHOR(S): Hogarth, Cathryn A.; Roy, Alison; Ebert, David L. [Reprint Author]
CORPORATE SOURCE: Russell Grimwade School of Biochemistry and Molecular Biology, University of Melbourne, Parkville, VIC, 3010, Australia
d.ebert@unimelb.edu.au
SOURCE: Comparative Biochemistry and Physiology Part B Biochemistry & Molecular Biology, (June 2003) Vol. 135B, No. 2, pp. 219-229. print.
ISSN: 1096-4959 (ISSN print).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 13 Aug 2003
Last Updated on STN: 13 Aug 2003
AB Mice and rats are naturally deficient in cholesteryl ester transfer protein (CETP) activity, although the reason behind the deficiency in activity is unknown. A search of mouse genome databases revealed sequences resembling 7 of the 16 human exons. However, these sequences could not code for a functional CETP. Analysis of the rat genome using

Southern blotting revealed sequences complementary to human CETP cDNA, but RNase protection assays were unable to detect any Cetp gene expression in liver, adipose, or muscle. A search of **rat whole-genome** shotgun databases revealed exon-like sequences that would be unable to code for a functional CETP. An Ap3s1 pseudogene lay immediately upstream of the CETP-like sequences in mouse, but was nearly identical to the functional gene and unlikely to have been inserted prior to mouse-rat divergence. In contrast, a deletion leading to a nonsense codon was found in the exon 11-like sequences of both rat and mouse and not in any other species. Thus, the lack of CETP activity in both the mouse and the rat is most likely due to an evolutionary event that occurred before these species diverged and not to altered regulation of the gene or function of the gene product.

L13 ANSWER 5 OF 6 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2002:368401 BIOSIS
DOCUMENT NUMBER: PREV200200368401
TITLE: Effects of dietary salt on gene expression in the rat kidney.
AUTHOR(S): Farjah, Mariam [Reprint author]; Li, Cheng; Yuzkova, Milana [Reprint author]; Geenen, David; Wong, Wing; Danziger, Robert S.
CORPORATE SOURCE: Cardiology, University of Illinois, Chicago, IL, USA
SOURCE: FASEB Journal, (March 20, 2002) Vol. 16, No. 4, pp. A421. print.
Meeting Info.: Annual Meeting of the Professional Research Scientists on Experimental Biology. New Orleans, Louisiana, USA. April 20-24, 2002.
CODEN: FAJOEC. ISSN: 0892-6638.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Jul 2002
Last Updated on STN: 3 Jul 2002

AB The present study was performed to determine changes in gene expression caused by increased dietary salt in the kidney to gain insight into molecular mechanisms of salt-adaptation. Sprague-Dawley rats (200-250 g) were placed on either 8% or 0.8% NaCl diets (n=3 in each group) for ten days. Transcriptional profiles were assessed with **rat whole genome** GeneChips (Affymetrix) and analyzed by DNA-Chip Analyzer (dChip). For selected genes, results were compared with real-time reverse transcription-polymerase chain reaction (RT/PCR) analysis. Mean blood pressures tended to be greater on the high salt-diet (150+/-12 mmHg versus 128+/-1), however, the difference was not statistically significant. We identified 26 genes with decreased expression and 4 genes with increased expression on the 8% versus 0.8% NaCl diet (t-test for the mean expression difference $P<0.05$) (range -5 to +5 fold change in expression). These included genes which have a high likelihood of being significant in salt-adaptation and blood pressure control on the basis of literature, as well as completely novel ones. We conclude that salt-adaptation in the kidney occurs, at least in part, through transcriptional regulation.

L13 ANSWER 6 OF 6 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN
ACCESSION NUMBER: 2003233447 EMBASE
TITLE: Genomic evidence for the absence of a functional cholesteryl ester transfer protein gene in mice and rats.
AUTHOR: Hogarth C.A.; Roy A.; Ebert D.L.
CORPORATE SOURCE: D.L. Ebert, Russell Grimwade Sch. Biochem./M., University of Melbourne, Parkville, Vic. 3010, Australia.
d.ebert@unimelb.edu.au
SOURCE: Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, (1 Jun 2003) Vol. 135, No. 2, pp.

219-229. .
Refs: 37
ISSN: 1096-4959 CODEN: CBPBB8
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 26 Jun 2003
Last Updated on STN: 26 Jun 2003

AB Mice and rats are naturally deficient in cholesteryl ester transfer protein (CETP) activity, although the reason behind the deficiency in activity is unknown. A search of mouse genome databases revealed sequences resembling 7 of the 16 human exons. However, these sequences could not code for a functional CETP. Analysis of the rat genome using Southern blotting revealed sequences complementary to human CETP cDNA, but RNase protection assays were unable to detect any Cetp gene expression in liver, adipose, or muscle. A search of **rat whole-genome** shotgun databases revealed exon-like sequences that would be unable to code for a functional CETP. An Ap3s1 pseudogene lay immediately upstream of the CETP-like sequences in mouse, but was nearly identical to the functional gene and unlikely to have been inserted prior to mouse-rat divergence. In contrast, a deletion leading to a nonsense codon was found in the exon 11-like sequences of both rat and mouse and not in any other species. Thus, the lack of CETP activity in both the mouse and the rat is most likely due to an evolutionary event that occurred before these species diverged and not to altered regulation of the gene or function of the gene product.

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Connection closed by remote host
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     (FILE 'HOME' ENTERED AT 15:51:20 ON 10 APR 2006)

     FILE 'MEDLINE, AGRICOLA, CABA, CAPLUS, BIOSIS, DISSABS, EMBASE' ENTERED
     AT 15:52:25 ON 10 APR 2006
L1           210 SEA ABB=ON  PLU=ON  RAT 230
L2            88 DUP REM L1 (122 DUPLICATES REMOVED)
L3            65 SEA ABB=ON  PLU=ON  L2 AND PY<2002
                 D L3 1-10 IBIB ABS
L4             3 SEA ABB=ON  PLU=ON  RAT GENOME U34 SET
                 D L4 1- TI
                 D L4 1- IBIB ABS
L5             0 SEA ABB=ON  PLU=ON  UNIGENE AND RAT AND BUILD 34
L6             9 SEA ABB=ON  PLU=ON  UNIGENE AND RAT AND BUILD
                 D L6 1- TI
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